- 1/12 -

## SEQUENCE LISTING

<110> TWINSTRAND THERAPEUTICS INC. BORGFORD, Thor BRAUN, Curtis PURAC, Admir STOLL, Dominik <120> GLYCOSYLATION VARIANTS OF RICIN-LIKE PROTEINS <130> 10447-42 <140> <141> <150> US 60/555,678 <151> 2004-03-24 <160> 6 <170> PatentIn version 3.3 <210> 1 <211> 530 <212> PRT <213> Artificial Sequence <220> <223> TST10088 Protein Sequence <400> 1 Glu Ala Glu Ala Ile Phe Pro Lys Gln Tyr Pro Ile Ile Gln Phe Thr 10 Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val 25 Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln Arg Phe Ile Leu Val 55 Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala Leu Asp Val 75 Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe 90 Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr His Leu Phe 100 105

Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp

- 2/12 -

Arg Leu Glu Gln Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met Arg Thr Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser Val Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln Arg Arg Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu Ile Pro Ile Ile Ala Leu Met Val Tyr Arg Cys Ser Pro Gln Gly Ile Ala Gly Gln Cys Met Asp Pro Glu Pro Ile Val Arg Ile Val Gly Arg Asn Gly Leu Cys Val Asp Val Arg Asp Gly Arg Phe His Asn Gly Asn Ala Ile Gln Leu Trp Pro Cys Lys Ser Asn Thr Asp Ala Asn Gln Leu Trp Thr Leu Lys Arg Asp Asn Thr Ile Arg Ser Asn Gly Lys Cys Leu Thr Thr Tyr Gly Tyr Ser Pro Gly Val Tyr Val Met Ile Tyr Asp Cys Asn Thr Ala Ala Thr Asp Ala Thr Arg Trp Gln Ile Trp Asp Asn Gly Thr Ile Ile Asn 

- 3/12 -

Pro Arg Ser Ser Leu Val Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr 370 380

Thr Leu Thr Val Gln Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp Leu 385 390 395 400

Pro Thr Gln Asn Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu Tyr
405 410 415

Gly Leu Cys Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp Cys 420 425 430

Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly Ser 435 440 445

Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser Asn 450 455 460

Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser Ser 465 470 475 480

Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn Leu Tyr 485 490 495

Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp Pro Ser Leu Lys Gln 500 505 510

Ile Ile Leu Tyr Pro Leu His Gly Asp Pro Asn Gln Ile Trp Leu Pro 515 520 525

Leu Phe 530

<210> 2

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> TST10092 Protein Sequence

<400> 2

Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val

- 4/12 -

Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala Leu Asp Val Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe Phe His Pro Asp Asn Glu Glu Asp Ala Glu Ala Ile Thr His Leu Phe Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu Glu Gln Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile 1.70 Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met Arg Thr Arg Ile Arg Tyr Asn Arg Ser Ala Pro Asp Pro Ser Val Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln Arg Arg Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu Ile Pro Ile Ile Ala Leu Met Val Tyr Arg Cys Ser Pro Gln Gly Ile Ala Gly Gln Cys 

WO 2005/090575

Met	Asp	Pro 275	Glu	Pro	Ile	Val	Arg 280	Ile	Val	Gly	Arg	Asn 285	Gly	Leu	Cys
Val	Asp 290	Val	Arg	Asp	Gly	Arg 295	Phe	His	Asn	Gly	Asn 300	Ala	Ile	Gln	Leu
Trp 305	Pro	Cys	Lys	Ser	Asn 310	Thr	Asp	Ala	Asn	Gln 315	Leu	Trp	Thr	Leu	Lys 320
Arg	Asp	Asn	Thr	Ile 325	Arg	Ser	Asn	Gly	Lys 330	Cys	Leu	Thr	Thr	Tyr 335	Gly
Tyr	Ser	Pro	Gly 340	Val	Tyr	Val	Met	Ile 345	Tyr	Asp	Cys	Asn	Thr 350	Ala	Ala
Thr	Asp	Ala 355	Thr	Arg	Trp	Gln	Ile 360	Trp	Asp	Asn	Gly	Thr 365	Ile	Ile	Asn
Pro	Arg 370	Ser	Ser	Leu	Val	Leu 375	Ala	Ala	Thr	Ser	Gly 380	Asn	Ser	Gly	Thr
Thr 385	Leu	Thr	Val	Gln	Thr 390	Asn	Ile	Tyr	Ala	Val 395	Ser	Gln	Gly	Trp	Leu 400
Pro	Thr	Asn	Asn	Thr 405	Gln	Pro	Phe	Val	Thr 410	Thr	Ile	Val	Gly	Leu 415	Tyr
Gly	Leu	Cys	Leu 420	Gln	Ala	Asn	Ser	Gly 425	Gln	Val	Trp	Ile	Glu 430	Asp	Cys
Ser	Ser	Glu 435	Lys	Ala	Glu	Gln	Gln 440	Trp	Ala	Leu	Tyr	Ala 445	Asp	Gly	Ser
Ile	Arg 450	Pro	Gln	Gln	Asn	Arg 455	Asp	Asn	Cys	Leu	Thr 460	Ser	Asp	Ser	Asn
Ile 465	Arg	Glu	Thr	Val	Val 470	Lys	Ile	Leu	Ser	Cys 475	Gly	Pro	Ala	Ser	Ser 480
Gly	Gln	Arg	Trp	Met 485	Phe	Lys	Asn	Asp	Gly 490	Thr	Ile	Leu	Asn	Leu 495	Tyr
Ser	Gly	Leu	Val 500	Leu	Asp	Val	Arg	Ala 505	ser	Asp	Pro	Ser	Leu 510	Lys	Gln

- 6/12 -

Ile Ile Leu Tyr Pro Leu His Gly Asp Pro Asn Gln Ile Trp Leu Pro 520

Leu Phe 530

<210> 3

<211> 531

<212> PRT <213> Artificial Sequence

<220>

<223> TST10147 Protein Sequence

<400> 3

Glu Ala Glu Ala Ile Phe Pro Lys Gln Tyr Pro Ile Ile Gln Phe Thr 5 1.0

Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile Arg Ala Val 20 25 30

Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His Glu Ile Pro Val 35

Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln Arg Phe Ile Leu Val 50 55 60

Glu Leu Ser Asn His Ala Glu Leu Ser Val Thr Leu Ala Leu Asp Val 70 75

Thr Asn Ala Tyr Val Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe 95

Phe His Pro Asp Asn Gln Glu Asp Ala Glu Ala Ile Thr His Leu Phe 100

Thr Asp Val Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp 115 120

Arg Leu Glu Gln Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly 130 135 140

Asn Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr 145 160

Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile 165 170

PCT/CA2005/000436

Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met 185 Arg Thr Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser Val 195 200 Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu 215 220 Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln Arg Arg Asn 230 235 Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu Ile Pro Ile Ile 250 Ala Leu Met Val Tyr Arg Cys Gly Ser Pro Gln Gly Ile Ala Gly Gln Cys Met Asp Pro Glu Pro Ile Val Arg Ile Val Gly Arg Asn Gly Leu 280 Cys Val Asp Val Arg Asp Gly Arg Phe His Asn Gly Asn Ala Ile Gln 295 300 Leu Trp Pro Cys Lys Ser Asn Thr Asp Ala Asn Gln Leu Trp Thr Leu 315 Lys Arg Asp Asn Thr Ile Arg Ser Asn Gly Lys Cys Leu Thr Thr Tyr 325 330 Gly Tyr Ser Pro Gly Val Tyr Val Met Ile Tyr Asp Cys Asn Thr Ala 340 345 Ala Thr Asp Ala Thr Arg Trp Gln Ile Trp Asp Asn Gly Thr Ile Ile 360 Asn Pro Arg Ser Ser Leu Val Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr Thr Leu Thr Val Gln Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp 390 Leu Pro Thr Gln Asn Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu 410

- 8/12 -

Tyr Gly Leu Cys Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp 420 Cys Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly 435 440 Ser Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser 450 455 460 Asn Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser 465 470 475 480 Ser Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn Leu 485 490 Tyr Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp Pro Ser Leu Lys 500 505 Gln Ile Ile Leu Tyr Pro Leu His Gly Asp Pro Asn Gln Ile Trp Leu 515 520 525 Pro Leu Phe 530 <210> 4 <211> 1707 <212> DNA <213> Artificial Sequence <220> <223> TST10088 DNA Insert Sequence <220> <221> prim\_transcript <222> (1)..(117) atgaaaccgg gaggaaatac tattgtaata tgggtgtatg cagtggcaac atggctttgt 60 tttggatcca cctcagggtg gtctttcaca ttagaggata acaacctcga gaaaagagag 120 gctgaagcta tattccccaa acaataccca attatacagt ttaccacagc gggtgccact 180 gtgcaaagct acacaaactt tatcagagct gttcgcggtc gtttaacaac tggagctgat 240 gtgagacatg aaataccagt gttgccaaac agagttggtt tgcctataaa ccaacggttt 300 attttagttg aactctcaaa tcatgcagag ctttctgtta cattagcgct ggatgtcacc 360 aatgcatatg tggtcggcta ccgtgctgga aatagcgcat atttctttca tcctgacaat 420

- 9/12 -

caggaagatg cagaagcaat cactcatctt ttcactgatg ttcaaaatcg atatacattc	480								
gcctttggtg gtaattatga tagacttgaa caacttgctg gtaatctgag agaaaatatc	540								
gagttgggaa atggtccact agaggaggct atctcagcgc tttattatta cagtactggt	600								
ggcactcagc ttccaactct ggctcgttcc tttataattt gcatccaaat gatttcagaa	660								
gcagcaagat tccaatatat tgagggagaa atgcgcacga gaattaggta caaccggaga	720								
tctgcaccag atcctagcgt aattacactt gagaatagtt gggggagact ttccactgca	780								
attcaagagt ctaaccaagg agcctttgct agtccaattc aactgcagag acgtaatggt	840								
tccaaattca gtgtgtacga tgtgagtata ttaatcccta tcatagctct catggtgtat	900								
agatgctctc cgcaaggaat tgcagggcag tgtatggatc ctgagcccat agtgcgtatc	960								
gtaggtcgaa atggtctatg tgttgatgtt agggatggaa gattccacaa cggaaacgca	1020								
atacagttgt ggccatgcaa .gtctaataca gatgcaaatc agctctggac tttgaaaaga	1080								
gacaatacta ttcgatctaa tggaaagtgt ttaactactt acgggtacag tccgggagtc	1140								
tatgtgatga tctatgattg caatactgct gcaactgatg ccacccgctg gcaaatatgg	1200								
gataatggaa ccatcataaa tcccagatct agtctagttt tagcagcgac atcagggaac	1260								
agtggtacca cacttacagt gcaaaccaac atttatgccg ttagtcaagg ttggcttcct	1320								
actcagaata cacaaccttt tgtgacaacc attgttgggc tatatggtct gtgcttgcaa	1380								
gcaaatagtg gacaagtatg gatagaggac tgtagcagtg aaaaggctga acaacagtgg	1440								
gctctttatg cagatggttc aatacgtcct cagcaaaacc gagataattg ccttacaagt	1500								
gattctaata tacgggaaac agttgtcaag atcctctctt gtggccctgc atcctctggc	1560								
caacgatgga tgttcaagaa tgatggaacc attttaaatt tgtatagtgg gttggtgtta	1620								
gatgtgaggg catcagatcc gagccttaaa caaatcattc tttaccctct ccatggtgac	1680								
ccaaaccaaa tatggttacc attattt	1707								
<pre> &lt;210&gt; 5 &lt;211&gt; 1707 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence  &lt;220&gt; &lt;223&gt; TST10092 DNA Insert Sequence  &lt;220&gt; &lt;221&gt; prim_transcript &lt;222&gt; (1)(117) &lt;400&gt; 5</pre>									
atgaaaccgg gaggaaatac tattgtaata tgggtgtatg cagtggcaac atggctttgt	60								

## - 10/12 -

tttggatcca	cctcagggtg	gtctttcaca	ttagaggata	acaacctcga	gaaaagagag	120
gctgaagcta	tattccccaa	acaataccca	attatacagt	ttaccacagc	gggtgccact	180
gtgcaaagct	acacaaactt	tatcagagct	gttcgcggtc	gtttaacaac	tggagctgat	240
gtgagacatg	aaataccagt	gttgccaaac	agagttggtt	tgcctataaa	ccaacggttt	300
attttagttg	aactctcaaa	tcatgcagag	ctttctgtta	cattagcgct	ggatgtcacc	360
aatgcatatg	tggtcggcta	ccgtgctgga	aatagcgcat	atttctttca	tcctgacaat	420
caggaagatg	cagaagcaat	cactcatctt	ttcactgatg	ttcaaaatcg	atatacattc	480
gcctttggtg	gtaattatga	tagacttgaa	caacttgctg	gtaatctgag	agaaaatatc	540
gagttgggaa	atggtccact	agaggaggct	atctcagcgc	tttattatta	cagtactggt	600
ggcactcagc	ttccaactct	ggctcgttcc	tttataattt	gcatccaaat	gatttcagaa	660
gcagcaagat	tccaatatat	tgagggagaa	atgcgcacga	gaattaggta	caaccggaga	720
tctgcaccag	atcctagcgt	aattacactt	gagaatagtt	gggggagact	ttccactgca	780
attcaagagt	ctaaccaagg	agcctttgct	agtccaattc	aactgcagag	acgtaatggt	840
tccaaattca	gtgtgtacga	tgtgagtata	ttaatcccta	tcatagctct	catggtgtat	900
agatgctctc	cgcaaggaat	tgcagggcag	tgtatggatc	ctgagcccat	agtgcgtatc	960
gtaggtcgaa	atggtctatg	tgttgatgtt	agggatggaa	gattccacaa	cggaaacgca	1020
atacagttgt	ggccatgcaa	gtctaataca	gatgcaaatc	agctctggac	tttgaaaaga	1080
gacaatacta	ttcgatctaa	tggaaagtgt	ttaactactt	acgggtacag	tccgggagtc	1140
tatgtgatga	tctatgattg	caatactgct	gcaactgatg	ccacccgctg	gcaaatatgg	1200
gataatggaa	ccatcataaa	tcccagatct	agtctagttt	tagcagcgac	atcagggaac	1260
agtggtacca	cacttacagt	gcaaaccaac	atttatgccg	ttagtcaagg	ttggcttcct	1320
actaataata	cacaaccttt	tgtgacaacc	attgttgggc	tatatggtct	gtgcttgcaa	1380
gcaaatagtg	gacaagtatg	gatagaggac	tgtagcagtg	aaaaggctga	acaacagtgg	1440
gctctttatg	cagatggttc	aatacgtcct	cagcaaaacc	gagataattg	ccttacaagt	1500
gattctaata	tacgggaaac	agttgtcaag	atcctctctt	gtggccctgc	atcctctggc	1560
caacgatgga	tgttcaagaa	tgatggaacc	attttaaatt	tgtatagtgg	gttggtgtta	1620
gatgtgaggg	catcagatcc	gagccttaaa	caaatcattc	tttaccctct	ccatggtgac	1680
ccaaaccaaa	tatggttacc	attattt				1707

<sup>&</sup>lt;210> 6 <211> 1710 <212> DNA <213> Artificial Sequence

<220> <223> TST10147 DNA Insert Sequence <220> <221> prim\_transcript <222> (1)..(117) <400> 6 atgaaaccgg gaggaaatac tattgtaata tgggtgtatg cagtggcaac atggctttgt 60 tttggatcca cctcagggtg gtctttcaca ttagaggata acaacctcga gaaaagagag 120 gctgaagcta tattccccaa acaataccca attatacagt ttaccacagc gggtgccact 180 gtgcaaagct acacaaactt tatcagagct gttcgcggtc gtttaacaac tggagctgat 240 gtgagacatg aaataccagt gttgccaaac agagttggtt tgcctataaa ccaacggttt 300 attttagttg aactctcaaa tcatgcagag ctttctgtta cattagcgct ggatgtcacc 360 aatgcatatg tggtcggcta ccgtgctgga aatagcgcat atttctttca tcctgacaat 420 caggaagatg cagaagcaat cactcatctt ttcactgatg ttcaaaatcg atatacattc 480 gcctttggtg gtaattatga tagacttgaa caacttgctg gtaatctgag agaaaatatc 540 gagttgggaa atggtccact agaggaggct atctcagcgc tttattatta cagtactggt 600 ggcactcagc ttccaactct ggctcgttcc tttataattt gcatccaaat gatttcagaa 660 gcagcaagat tccaatatat tgagggagaa atgcgcacga gaattaggta caaccggaga 720 tctgcaccag atcctagcgt aattacactt gagaatagtt gggggagact ttccactgca 780 attcaagagt ctaaccaagg agcctttgct agtccaattc aactgcagag acgtaatggt 840 tccaaattca gtgtgtacga tgtgagtata ttaatcccta tcatagctct catggtgtat 900 agatgcggtt ctccgcaagg aattgcaggg cagtgtatgg atcctgagcc catagtgcgt 960 atcgtaggtc gaaatggtct atgtgttgat gttagggatg gaagattcca caacggaaac 1020 gcaatacagt tgtggccatg caagtctaat acagatgcaa atcagctctg gactttgaaa 1080 agagacaata ctattcgatc taatggaaag tgtttaacta cttacgggta cagtccggga 1140 gtctatgtga tgatctatga ttgcaatact gctgcaactg atgccacccg ctggcaaata 1200 1260 aacagtggta ccacacttac agtgcaaacc aacatttatg ccgttagtca aggttggctt 1320 cctactcaga atacacaacc ttttgtgaca accattgttg ggctatatgg tctgtgcttg 1380 caagcaaata gtggacaagt atggatagag gactgtagca gtgaaaaggc tgaacaacag 1440 tgggctcttt atgcagatgg ttcaatacgt cctcagcaaa accgagataa ttgccttaca 1500 agtgattcta atatacggga aacagttgtc aagatcctct cttgtggccc tgcatcctct 1560

## - 12/12 -

ggccaacgat	ggatgttcaa	gaatgatgga	accattttaa	atttgtatag	tgggttggtg	1620
ttagatgtga	gggcatcaga	teegageett	aaacaaatca	ttctttaccc	tctccatggt	1680
gacccaaacc	aaatatggtt	accattattt				1710